

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/SS6,221  
Source: IFWP  
Date Processed by STIC: 12/8/06

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IFWP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/556,221

DATE: 12/08/2006

TIME: 09:06:01

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\12082006\J556221.raw

```

3 <110> APPLICANT: Universite Laval
4     De Koninck, Yves
5     De Koninck, Paul
6     Coull, Jeffrey
8 <120> TITLE OF INVENTION: CNS chloride modulation and uses thereof
10 <130> FILE REFERENCE: 85409-29
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/556,221
C--> 12 <141> CURRENT FILING DATE: 2005-11-09
12 <150> PRIOR APPLICATION NUMBER: US 60/470,885
13 <151> PRIOR FILING DATE: 2003-05-16
15 <160> NUMBER OF SEQ ID NOS: 8
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 5907
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(3351)
29 <400> SEQUENCE: 1
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31 Met Pro Asn Asn Leu Thr Asp Cys Glu Asp Gly Asp Gly Gly Ala Asn
32 1          5          10          15
34 ccg ggt gat ggc aac ccc aag gaa agc agt ccc ttc atc aac agc acc      96
35 Pro Gly Asp Gly Asn Pro Lys Glu Ser Ser Pro Phe Ile Asn Ser Thr
36          20          25          30
38 gac aca gag aag gga aag gag tat gat ggc aag aac atg gcc ttg ttt      144
39 Asp Thr Glu Lys Gly Lys Glu Tyr Asp Gly Lys Asn Met Ala Leu Phe
40          35          40          45
42 gag gag gag atg gac acc agc cct atg gtg tcc tcc ttg ctc agt ggc      192
43 Glu Glu Glu Met Asp Thr Ser Pro Met Val Ser Ser Leu Leu Ser Gly
44          50          55          60
46 ctg gcc aac tac acc aac ctg ccc cag gga agt agg gag cat gaa gag      240
47 Leu Ala Asn Tyr Thr Asn Leu Pro Gln Gly Ser Arg Glu His Glu Glu
48 65          70          75          80
50 gca gaa aac aat gag ggt gga aaa aag aag ccg gtg cag gcc cca cgc      288
51 Ala Glu Asn Asn Glu Gly Gly Lys Lys Lys Pro Val Gln Ala Pro Arg
52          85          90          95
54 atg ggc acc ttc atg ggc gtg tac ctg ccg tgc ctg cag aac atc ttt      336
55 Met Gly Thr Phe Met Gly Val Tyr Leu Pro Cys Leu Gln Asn Ile Phe
56          100         105         110
58 ggc gtc atc ctc ttc ctg cgg ctc acc tgg gtg gtg ggc att gca ggc      384
59 Gly Val Ile Leu Phe Leu Arg Leu Thr Trp Val Val Gly Ile Ala Gly

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60	115	120	125	
62	atc atg gag tcc ttc tgc atg gtg ttc atc tgc tgc tcc tgt acg atg	432		
63	Ile Met Glu Ser Phe Cys Met Val Phe Ile Cys Cys Ser Cys Thr Met			
64	130	135	140	
66	ctc acg gcc atc tcc atg agt gca att gca acg aat ggt gtt gtg cct	480		
67	Leu Thr Ala Ile Ser Met Ser Ala Ile Ala Thr Asn Gly Val Val Pro			
68	145	150	155	160
70	gct ggt ggc tcc tac tac atg att tcc agg tct ctg ggc cca gag ttt	528		
71	Ala Gly Gly Ser Tyr Tyr Met Ile Ser Arg Ser Leu Gly Pro Glu Phe			
72	165	170	175	
74	ggg ggt gcc gtg ggc ctc tgc ttc tac ctg ggc act acc ttt gca gga	576		
75	Gly Gly Ala Val Gly Leu Cys Phe Tyr Leu Gly Thr Thr Phe Ala Gly			
76	180	185	190	
78	gcc atg tac atc ctg ggc acc atc gaa atc ctg ctg gct tac ctc ttc	624		
79	Ala Met Tyr Ile Leu Gly Thr Ile Glu Ile Leu Leu Ala Tyr Leu Phe			
80	195	200	205	
82	cca gcc atg gcc atc ttc aag gca gaa gat gcc agt ggg gag gca gca	672		
83	Pro Ala Met Ala Ile Phe Lys Ala Glu Asp Ala Ser Gly Glu Ala Ala			
84	210	215	220	
86	gcc atg ctg aac aac atg cgt gtt tac ggc acc tgt gtg ctc acc tgc	720		
87	Ala Met Leu Asn Asn Met Arg Val Tyr Gly Thr Cys Val Leu Thr Cys			
88	225	230	235	240
90	atg gcc act gtg gtg ttt gtg ggt gtc aag tat gtc aac aag ttt gcc	768		
91	Met Ala Thr Val Val Phe Val Gly Val Lys Tyr Val Asn Lys Phe Ala			
92	245	250	255	
94	ctt gtc ttc ctg ggt tgt gtc atc ctc tcc atc ctg gcc atc tat gct	816		
95	Leu Val Phe Leu Gly Cys Val Ile Leu Ser Ile Leu Ala Ile Tyr Ala			
96	260	265	270	
98	ggg gtc atc aag tct gcc ttc gac cca ccc aac ttc ccg atc tgc ctc	864		
99	Gly Val Ile Lys Ser Ala Phe Asp Pro Pro Asn Phe Pro Ile Cys Leu			
100	275	280	285	
102	ctg ggt aac cgc acg ctg tct cgc cat ggc ttt gat gtc tgt gcc aag	912		
103	Leu Gly Asn Arg Thr Leu Ser Arg His Gly Phe Asp Val Cys Ala Lys			
104	290	295	300	
106	ctg gct tgg gaa gga aat gag acg gtg acc aca cgg cta tgg ggc ctt	960		
107	Leu Ala Trp Glu Gly Asn Glu Thr Val Thr Thr Arg Leu Trp Gly Leu			
108	305	310	315	320
110	ttc tgc tcc tct cgc ttc ctc aac gcc acc tgt gat gaa tac ttc acc	1008		
111	Phe Cys Ser Ser Arg Phe Leu Asn Ala Thr Cys Asp Glu Tyr Phe Thr			
112	325	330	335	
114	cga aac aat gtc aca gag atc cag ggc atc cct ggt gct gcc agt ggc	1056		
115	Arg Asn Asn Val Thr Glu Ile Gln Gly Ile Pro Gly Ala Ala Ser Gly			
116	340	345	350	
118	ctc atc aaa gag aac ctc tgg agc tcc tac ctg acc aag ggc gtg att	1104		
119	Leu Ile Lys Glu Asn Leu Trp Ser Ser Tyr Leu Thr Lys Gly Val Ile			
120	355	360	365	
122	gtg gag agg agt ggg atg acc tcg gtg ggc ctg gcc gat ggc act cct	1152		
123	Val Glu Arg Ser Gly Met Thr Ser Val Gly Leu Ala Asp Gly Thr Pro			
124	370	375	380	

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126	atc	gac	atg	gac	cac	cct	tat	gtc	ttc	agt	gat	atg	acc	tcc	tac	ttc	1200
127	Ile	Asp	Met	Asp	His	Pro	Tyr	Val	Phe	Ser	Asp	Met	Thr	Ser	Tyr	Phe	
128	385					390					395					400	
130	acc	ctg	ctg	gtt	ggc	atc	tac	ttc	ccc	tca	gtc	aca	ggg	atc	atg	gct	1248
131	Thr	Leu	Leu	Val	Gly	Ile	Tyr	Phe	Pro	Ser	Val	Thr	Gly	Ile	Met	Ala	
132					405					410					415		
134	ggt	tct	aac	cgc	tct	ggg	gac	ctg	agg	gat	gcc	cag	aag	tca	atc	ccc	1296
135	Gly	Ser	Asn	Arg	Ser	Gly	Asp	Leu	Arg	Asp	Ala	Gln	Lys	Ser	Ile	Pro	
136				420					425					430			
138	act	ggc	acc	atc	ctg	gcc	atc	gcc	acc	acc	tct	gct	gtc	tac	atc	agc	1344
139	Thr	Gly	Thr	Ile	Leu	Ala	Ile	Ala	Thr	Thr	Ser	Ala	Val	Tyr	Ile	Ser	
140			435					440					445				
142	tcc	gtt	gtt	ctg	ttt	ggg	gcc	tgc	att	gag	ggg	gtc	gtc	ctg	cgg	gac	1392
143	Ser	Val	Val	Leu	Phe	Gly	Ala	Cys	Ile	Glu	Gly	Val	Val	Leu	Arg	Asp	
144		450					455				460						
146	aag	ttt	ggc	gaa	gct	gtg	aat	ggc	aac	ctc	gtg	gtg	ggc	act	ctg	gcc	1440
147	Lys	Phe	Gly	Glu	Ala	Val	Asn	Gly	Asn	Leu	Val	Val	Gly	Thr	Leu	Ala	
148	465					470				475						480	
150	tgg	cca	tct	cca	tgg	gta	att	gtc	atc	gga	tcc	ttc	ttc	tcc	acc	tgt	1488
151	Trp	Pro	Ser	Pro	Trp	Val	Ile	Val	Ile	Gly	Ser	Phe	Phe	Ser	Thr	Cys	
152				485						490					495		
154	ggg	gct	ggg	ctg	cag	agc	ctc	acg	ggg	gcc	cca	cgc	ctg	ctg	cag	gcc	1536
155	Gly	Ala	Gly	Leu	Gln	Ser	Leu	Thr	Gly	Ala	Pro	Arg	Leu	Leu	Gln	Ala	
156				500					505					510			
158	atc	tcg	agg	gat	ggc	att	gtg	ccc	ttc	ctg	cag	gtc	ttt	ggc	cat	ggc	1584
159	Ile	Ser	Arg	Asp	Gly	Ile	Val	Pro	Phe	Leu	Gln	Val	Phe	Gly	His	Gly	
160			515					520					525				
162	aag	gcc	aat	gga	gag	ccg	acc	tgg	gcc	ctg	ctc	ctg	act	gcc	tgc	atc	1632
163	Lys	Ala	Asn	Gly	Glu	Pro	Thr	Trp	Ala	Leu	Leu	Leu	Thr	Ala	Cys	Ile	
164		530					535				540						
166	tgc	gag	att	ggc	atc	ctc	att	gca	tcc	ctc	gac	gag	gtg	gcc	ccc	atc	1680
167	Cys	Glu	Ile	Gly	Ile	Leu	Ile	Ala	Ser	Leu	Asp	Glu	Val	Ala	Pro	Ile	
168	545					550				555						560	
170	ctc	tct	atg	ttc	ttc	ctg	atg	tgc	tac	atg	ttt	gtg	aat	ctg	gcc	tgt	1728
171	Leu	Ser	Met	Phe	Phe	Leu	Met	Cys	Tyr	Met	Phe	Val	Asn	Leu	Ala	Cys	
172				565						570					575		
174	gca	gtg	cag	acg	ctg	ctg	agg	aca	ccc	aac	tgg	agg	cca	cgc	ttt	cga	1776
175	Ala	Val	Gln	Thr	Leu	Leu	Arg	Thr	Pro	Asn	Trp	Arg	Pro	Arg	Phe	Arg	
176				580					585					590			
178	tat	tac	cac	tgg	acc	ctc	tcc	ttc	ctg	ggc	atg	agc	ctc	tgc	ctg	gcc	1824
179	Tyr	Tyr	His	Trp	Thr	Leu	Ser	Phe	Leu	Gly	Met	Ser	Leu	Cys	Leu	Ala	
180			595					600					605				
182	ctc	atg	ttc	atc	tgc	tcc	tgg	tat	tat	gca	ctg	gta	gcc	atg	ctc	att	1872
183	Leu	Met	Phe	Ile	Cys	Ser	Trp	Tyr	Tyr	Ala	Leu	Val	Ala	Met	Leu	Ile	
184		610					615					620					
186	gct	gga	ctc	atc	tac	aag	tac	att	gag	tac	cgt	ggg	gca	gag	aag	gag	1920
187	Ala	Gly	Leu	Ile	Tyr	Lys	Tyr	Ile	Glu	Tyr	Arg	Gly	Ala	Glu	Lys	Glu	
188	625					630				635						640	
190	tgg	ggc	gat	ggg	ata	cga	ggt	ctg	tct	ctc	agt	gcg	gct	cgc	tat	gcc	1968

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191	Trp	Gly	Asp	Gly	Ile	Arg	Gly	Leu	Ser	Leu	Ser	Ala	Ala	Arg	Tyr	Ala	
192					645					650					655		
194	ctc	tta	cgc	ctg	gag	gaa	ggg	ccc	cca	cac	acc	aag	aac	tgg	agg	cca	2016
195	Leu	Leu	Arg	Leu	Glu	Glu	Gly	Pro	Pro	His	Thr	Lys	Asn	Trp	Arg	Pro	
196				660					665					670			
198	cag	ctg	ctg	gtg	ctg	gtg	cgt	gtg	gac	caa	gac	cag	aat	gtg	gtg	cac	2064
199	Gln	Leu	Leu	Val	Leu	Val	Arg	Val	Asp	Gln	Asp	Gln	Asn	Val	Val	His	
200			675					680					685				
202	ccc	cag	ctg	ctc	tca	ctg	acc	tcc	cag	ctg	aag	gca	ggg	aag	ggc	ctg	2112
203	Pro	Gln	Leu	Leu	Ser	Leu	Thr	Ser	Gln	Leu	Lys	Ala	Gly	Lys	Gly	Leu	
204		690						695				700					
206	acc	atc	gtg	ggc	tct	gtc	ctt	gag	ggc	acc	ttt	ctg	gaa	aat	cat	cca	2160
207	Thr	Ile	Val	Gly	Ser	Val	Leu	Glu	Gly	Thr	Phe	Leu	Glu	Asn	His	Pro	
208	705					710				715					720		
210	cag	gcc	cag	cgg	gca	gaa	gag	tct	atc	agg	cgc	ctg	atg	gag	gca	gag	2208
211	Gln	Ala	Gln	Arg	Ala	Glu	Glu	Ser	Ile	Arg	Arg	Leu	Met	Glu	Ala	Glu	
212				725						730				735			
214	aag	gtg	aag	ggc	ttc	tgc	cag	gtg	gtg	atc	tcc	tcc	aac	ttg	cgt	gat	2256
215	Lys	Val	Lys	Gly	Phe	Cys	Gln	Val	Val	Ile	Ser	Ser	Asn	Leu	Arg	Asp	
216			740						745				750				
218	ggc	gtg	tcc	cat	ctg	atc	cag	tcc	ggg	ggc	ctc	ggg	ggg	ctg	cag	cac	2304
219	Gly	Val	Ser	His	Leu	Ile	Gln	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Gln	His	
220			755					760				765					
222	aac	act	gtg	ctt	gtt	ggc	tgg	ccc	cgc	aac	tgg	cgc	cag	aag	gaa	gat	2352
223	Asn	Thr	Val	Leu	Val	Gly	Trp	Pro	Arg	Asn	Trp	Arg	Gln	Lys	Glu	Asp	
224		770					775			780							
226	cat	cag	acg	tgg	agg	aac	ttc	att	gag	ctg	gtc	cgg	gaa	acc	aca	gct	2400
227	His	Gln	Thr	Trp	Arg	Asn	Phe	Ile	Glu	Leu	Val	Arg	Glu	Thr	Thr	Ala	
228	785					790				795					800		
230	ggc	cac	tta	gcc	ctg	ctg	gtc	acc	aag	aac	gtt	tcc	atg	ttt	cct	ggg	2448
231	Gly	His	Leu	Ala	Leu	Leu	Val	Thr	Lys	Asn	Val	Ser	Met	Phe	Pro	Gly	
232				805						810				815			
234	aac	cct	gag	cgc	ttc	tct	gag	ggc	agc	atc	gac	gtt	tgg	tgg	att	gtg	2496
235	Asn	Pro	Glu	Arg	Phe	Ser	Glu	Gly	Ser	Ile	Asp	Val	Trp	Trp	Ile	Val	
236			820						825				830				
238	cac	gat	gga	ggc	atg	ctc	atg	ctg	ctg	ccc	ttc	ctg	ctg	cgg	cac	cac	2544
239	His	Asp	Gly	Gly	Met	Leu	Met	Leu	Leu	Pro	Phe	Leu	Leu	Arg	His	His	
240			835					840				845					
242	aag	gtc	tgg	cgg	aag	tgc	aag	atg	cgt	atc	ttc	act	gtg	gcc	cag	atg	2592
243	Lys	Val	Trp	Arg	Lys	Cys	Lys	Met	Arg	Ile	Phe	Thr	Val	Ala	Gln	Met	
244		850					855			860							
246	gat	gac	aat	agc	atc	cag	atg	aag	aag	gat	ctg	acc	aca	ttt	ctg	tat	2640
247	Asp	Asp	Asn	Ser	Ile	Gln	Met	Lys	Lys	Asp	Leu	Thr	Thr	Phe	Leu	Tyr	
248	865					870				875				880			
250	cat	tta	cgc	atc	act	gcg	gag	gtc	gag	gtg	gtg	gag	atg	cat	gag	agc	2688
251	His	Leu	Arg	Ile	Thr	Ala	Glu	Val	Glu	Val	Val	Glu	Met	His	Glu	Ser	
252				885						890				895			
254	gac	atc	tca	gct	tac	acc	tat	gag	aag	acg	ttg	gtg	atg	gag	cag	cgt	2736
255	Asp	Ile	Ser	Ala	Tyr	Thr	Tyr	Glu	Lys	Thr	Leu	Val	Met	Glu	Gln	Arg	



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256	900	905	910	
258	tcc cag atc ctc aaa cag atg cat tta acc aag aat gag cgg gag cgg	2784		
259	Ser Gln Ile Leu Lys Gln Met His Leu Thr Lys Asn Glu Arg Glu Arg			
260	915	920	925	
262	gag atc cag agt atc aca gat gag tca cga ggc tca atc cgg aga aag	2832		
263	Glu Ile Gln Ser Ile Thr Asp Glu Ser Arg Gly Ser Ile Arg Arg Lys			
264	930	935	940	
266	aat cca gcc aac acg cgg ctc cgc ctg aac gtc cca gaa gag acg gct	2880		
267	Asn Pro Ala Asn Thr Arg Leu Arg Leu Asn Val Pro Glu Glu Thr Ala			
268	945	950	955	960
270	ggt gac agt gaa gag aag cca gag gag gag gtg cag ctg atc cac gat	2928		
271	Gly Asp Ser Glu Glu Lys Pro Glu Glu Glu Val Gln Leu Ile His Asp			
272	965	970	975	
274	cag agt gct ccc agc tgc ccc agc agc tcc ccg tcc cca ggg gag gag	2976		
275	Gln Ser Ala Pro Ser Cys Pro Ser Ser Ser Pro Ser Pro Gly Glu Glu			
276	980	985	990	
278	cct gag ggg gaa ggg gag aca gat ccg gag aag gtg cat ctc acc tgg	3024		
279	Pro Glu Gly Glu Gly Glu Thr Asp Pro Glu Lys Val His Leu Thr Trp			
280	995	1000	1005	
282	acc aag gac aag tcg gtg gca gag aag aat aag ggc ccc agt cct	3069		
283	Thr Lys Asp Lys Ser Val Ala Glu Lys Asn Lys Gly Pro Ser Pro			
284	1010	1015	1020	
286	gtc tcc tct gag ggc atc aag gac ttc ttc agc atg aag ccg gag	3114		
287	Val Ser Ser Glu Gly Ile Lys Asp Phe Phe Ser Met Lys Pro Glu			
288	1025	1030	1035	
290	tgg gag aac ttg aac cag tcc aac gtg cgg cgc atg cac acg gcc	3159		
291	Trp Glu Asn Leu Asn Gln Ser Asn Val Arg Arg Met His Thr Ala			
292	1040	1045	1050	
294	gtg cgg ctg aac gag gtc atc gtg aag aaa tcc cgg gac gcc aag	3204		
295	Val Arg Leu Asn Glu Val Ile Val Lys Lys Ser Arg Asp Ala Lys			
296	1055	1060	1065	
298	ctt gtt ttg ctc aac atg cct ggg cct ccc cgc aac cgc aat ggt	3249		
299	Leu Val Leu Leu Asn Met Pro Gly Pro Pro Arg Asn Arg Asn Gly			
300	1070	1075	1080	
302	gat gaa aac tac atg gag ttt ctc gag gtc ctc aca gag cac ctg	3294		
303	Asp Glu Asn Tyr Met Glu Phe Leu Glu Val Leu Thr Glu His Leu			
304	1085	1090	1095	
306	gac cgg gtg atg ctg gtc cgc ggt ggt ggc cga gag gtc atc acc	3339		
307	Asp Arg Val Met Leu Val Arg Gly Gly Gly Arg Glu Val Ile Thr			
308	1100	1105	1110	
310	atc tac tcc tga gaaccagggtc ctgccacccg ggcccagagcg cgcccggccc	3391		
311	Ile Tyr Ser			
312	1115			
314	gcggctccgg agccctcgcc gcgccccccg ccgctgtcac cgtttacata cagaccctgt	3451		
316	gcccggtgtcc tggcccctta ccccgctgcc tgaagcccgg aggccacgcc tggtggggct	3511		
318	gattcggaga gggcgccccg ccgcgcagag accagagctc ctcaagtcca gtttggcccc	3571		
320	tgggtcttcg ctgccctttt tctaagcccg gcctcgtctc gccggaggag acgctgcaat	3631		
322	aaaggttggg agaaggcgcg gaaaggagag gagctggggc cttggggacc cccaggtagt	3691		
324	ccatgcggcc cattcctccc cttcccactc ccgccgcggt cctcgctctg cgctcctccg	3751		

**VERIFICATION SUMMARY**

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date